

0500/0000 #2



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/055,061

DATE: 02/07/2002

TIME: 11:09:48

Input Set : N:\Crf3\RULE60\10055061.raw
 Output Set: N:\CRF3\02072002\J055061.raw

1 <110> APPLICANT: Bertin, John
 2 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 3 PROTEIN FAMILY AND USES THEREOF
 4 <130> FILE REFERENCE: 07334-076001
 5 <140> CURRENT APPLICATION NUMBER: 10/055,061
 6 <141> CURRENT FILING DATE: 2002-01-22
 8 <150> PRIOR APPLICATION NUMBER: US/09/099,041A
 9 <151> PRIOR FILING DATE: 1998-06-17
 12 <150> PRIOR APPLICATION NUMBER: 09/019,942
 13 <151> PRIOR FILING DATE: 1998-02-06
 14 <160> NUMBER OF SEQ ID NOS: 37
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1931
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (214)...(1833)
 24 <400> SEQUENCE: 1
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 26 tgggcgcctt cgtgacctag tttgcgggg caaaaagggt ctggccggcc tcgctcgatc 120
 27 aggggcgtat ctgggcgcct gagcgcggcg tgggagccctt gggagccggcc gcagcagggg 180
 28 gcacacccgg aaccggcctg agcgcgggg acc atg aac ggg gag gcc atc tgc 234
 Met Asn Gly Glu Ala Ile Cys
 30 1 5
 31 agc gcc ctg ccc acc att ccc tac cac aaa ctc gcc gac ctg cgc tac 282
 Ser Ala Leu Pro Thr Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr
 32 10 15 20
 34 ctg agc cgc ggc gcc tct ggc act gtg tcg tcc gcc cgc cac gca gac 330
 35 Leu Ser Arg Gly Ala Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp
 36 25 30 35
 37 tgg cgc gtc cag gtg gcc gtg aag cac ctg cac atc cac act ccg ctg 378
 Trp Arg Val Gln Val Ala Val Lys His Leu His Ile His Thr Pro Leu
 39 40 45 50 55
 40 ctc gac agt gaa aga aag gat gtc tta aga gaa gct gaa att tta cac 426
 41 Leu Asp Ser Glu Arg Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His
 42 60 65 70
 43 aaa gct aga ttt agt tac att ctt cca att ttg gga att tgc aat gag 474
 Lys Ala Arg Phe Ser Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu
 44 75 80 85
 46 cct gaa ttt ttg gga ata gtt act gaa tac atg cca aat gga tca tta 522
 Pro Glu Phe Leu Gly Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu
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48	90	95	100	
49	aat gaa ctc cta cat agg aaa act gaa tat cct gat gtt gct tgg cca			570
50	Asn Glu Leu Leu His Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro			
51	105 110 115			
52	ttg aga ttt cgc atc ctg cat gaa att gcc ctt ggt gta aat tac ctg			618
53	Leu Arg Phe Arg Ile Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu			
54	120 125 130 135			
55	cac aat atg act cct cct tta ctt cat cat gac ttg aag act cag aat			666
56	His Asn Met Thr Pro Pro Leu Leu His His Asp Leu Lys Thr Gln Asn			
57	140 145 150			
58	atc tta ttg gac aat gaa ttt cat gtt aag att gca gat ttt ggt tta			714
59	Ile Leu Leu Asp Asn Glu Phe His Val Lys Ile Ala Asp Phe Gly Leu			
60	155 160 165			
61	tca aag tgg cgc atg atg tcc ctc tca cag tca cga agt agc aaa tct			762
62	Ser Lys Trp Arg Met Met Ser Leu Ser Gln Ser Arg Ser Ser Lys Ser			
63	170 175 180			
64	gca cca gaa gga ggg aca att atc tat atg cca cct gaa aac tat gaa			810
65	Ala Pro Glu Gly Gly Thr Ile Ile Tyr Met Pro Pro Glu Asn Tyr Glu			
66	185 190 195			
67	cct gga caa aaa tca agg gcc agt atc aag cac gat ata tat agc tat			858
68	Pro Gly Gln Lys Ser Arg Ala Ser Ile Lys His Asp Ile Tyr Ser Tyr			
69	200 205 210 215			
70	gca gtt atc aca tgg gaa gtg tta tcc aga aaa cag cct ttt gaa gat			906
71	Ala Val Ile Thr Trp Glu Val Leu Ser Arg Lys Gln Pro Phe Glu Asp			
72	220 225 230			
73	gtc acc aat cct ttg cag ata atg tat agt gtg tca caa gga cat cga			954
74	Val Thr Asn Pro Leu Gln Ile Met Tyr Ser Val Ser Gln Gly His Arg			
75	235 240 245			
76	cct gtt att aat gaa gaa agt ttg cca tat gat ata cct cac cga gca			1002
77	Pro Val Ile Asn Glu Glu Ser Leu Pro Tyr Asp Ile Pro His Arg Ala			
78	250 255 260			
79	cgt atg atc tct cta ata gaa agt gga tgg gca caa aat cca gat gaa			1050
80	Arg Met Ile Ser Leu Ile Glu Ser Gly Trp Ala Gln Asn Pro Asp Glu			
81	265 270 275			
82	aga cca tct ttc tta aaa tgt tta ata gaa ctt gaa cca gtt ttg aga			1098
83	Arg Pro Ser Phe Leu Lys Cys Leu Ile Glu Leu Glu Pro Val Leu Arg			
84	280 285 290 295			
85	aca ttt gaa gag ata act ttt ctt gaa gct gtt att cag cta aag aaa			1146
86	Thr Phe Glu Ile Thr Phe Leu Glu Ala Val Ile Gln Leu Lys Lys			
87	300 305 310			
88	aca aag tta cag agt gtt tca agt gcc att cac cta tgt gac aag aag			1194
89	Thr Lys Leu Gln Ser Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys			
90	315 320 325			
91	aaa atg gaa tta tct ctg aac ata cct gta aat cat ggt cca caa gag			1242
92	Lys Met Glu Leu Ser Leu Asn Ile Pro Val Asn His Gly Pro Gln Glu			
93	330 335 340			
94	gaa tca tgt gga tcc tct cag ctc cat gaa aat agt ggt tct cct gaa			1290
95	Glu Ser Cys Gly Ser Ser Gln Leu His Glu Asn Ser Gly Ser Pro Glu			
96	345 350 355			

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97	act tca agg tcc ctg cca gct cct caa gac aat gat ttt tta tct aga	1338
98	Thr Ser Arg Ser Leu Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg	
99	360 365 370 375	
100	aaa gct caa gac tgt tat ttt atg aag ctg cat cac tgt cct gga aat	1386
101	Lys Ala Gln Asp Cys Tyr Phe Met Lys Leu His His Cys Pro Gly Asn	
102	380 385 390	
103	cac agt tgg gat agc acc att tct gga tct caa agg gct gca ttc tgt	1434
104	His Ser Trp Asp Ser Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys	
105	395 400 405	
106	gat cac aag acc att cca tgc tct tca gca ata ata aat cca ctc tca	1482
107	Asp His Lys Thr Ile Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser	
108	410 415 420	
109	act gca gga aac tca gaa cgt ctg cag cct ggt ata gcc cag cag tgg	1530
110	Thr Ala Gly Asn Ser Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp	
111	425 430 435	
112	atc cag agc aaa agg gaa gac att gtg aac caa atg aca gaa gcc tgc	1578
113	Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys	
114	440 445 450 455	
115	ctt aac cag tcg cta gat gcc ctt ctg tcc agg gac ttg atc atg aaa	1626
116	Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys	
117	460 465 470	
118	gag gac tat gaa ctt gtt agt acc aag cct aca agg acc tca aaa gtc	1674
119	Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val	
120	475 480 485	
121	aga caa tta cta gac act act gac atc caa gga gaa gaa ttt gcc aaa	1722
122	Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys	
123	490 495 500	
124	gtt ata gta caa aaa ttg aaa gat aac aaa caa atg ggt ctt cag cct	1770
125	Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro	
126	505 510 515	
127	tac ccg gaa ata ctt gtg gtt tct aga tca cca tct tta aat tta ctt	1818
128	Tyr Pro Glu Ile Leu Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu	
129	520 525 530 535	
130	caa aat aaa agc atg taagtgactg tttttcaaga agaaatgtgt ttcataaaag	1873
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133	gatattttata aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa	1931
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136 <211>	LENGTH: 540	
137 <212>	TYPE: PRT	
138 <213>	ORGANISM: Homo sapiens	
139 <400>	SEQUENCE: 2	
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142	Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val	
143	20 25 30	
144	Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His	
145	35 40 45	
146	Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu	

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147	50	55	60													
148	Arg	Glu	Ala	Glu	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro
149	65		70		75											80
150	Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu
151					85					90					95	
152	Tyr	Met	Pro	Asn	Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu
153					100				105					110		
154	Tyr	Pro	Asp	Val	Ala	Trp	Pro	Leu	Arg	Phe	Arg	Ile	Leu	His	Glu	Ile
155					115			120				125				
156	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	Pro	Leu	Leu	His
157					130			135			140					
158	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Asp	Asn	Glu	Phe	His	Val	
159					145			150		155				160		
160	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser
161					165			170				175				
162	Gln	Ser	Arg	Ser	Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr
163					180			185			190					
164	Met	Pro	Pro	Glu	Asn	Tyr	Glu	Pro	Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile
165					195			200			205					
166	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	Glu	Val	Leu	Ser
167					210			215			220					
168	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr
169					225			230		235				240		
170	Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro
171					245			250			255					
172	Tyr	Asp	Ile	Pro	His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Glu	Ser	Gly
173					260			265			270					
174	Trp	Ala	Gln	Asn	Pro	Asp	Glu	Arg	Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile
175					275			280			285					
176	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Glu	Ile	Thr	Phe	Leu	Glu
177					290			295			300					
178	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala
179					305			310		315				320		
180	Ile	His	Leu	Cys	Asp	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	
181					325			330			335					
182	Val	Asn	His	Gly	Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His
183					340			345			350					
184	Glu	Asn	Ser	Gly	Ser	Pro	Glu	Thr	Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln
185					355			360			365					
186	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	Tyr	Phe	Met	Lys
187					370			375			380					
188	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly
189					385			390		395				400		
190	Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser
191					405			410			415					
192	Ala	Ile	Ile	Asn	Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Glu	Arg	Leu	Gln
193					420			425			430					
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195					435			440			445					

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196 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
 197 450 455 460
 198 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
 199 465 470 475 480
 200 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
 201 485 490 495
 202 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
 203 500 505 510
 204 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
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 212 <213> ORGANISM: Homo sapiens
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216	cgcgtccagg	tggccgtgaa	gcacacctgc	atccacactc	cgctgctcga	cagtggaaaaga	180
217	aaggatgtct	taagagaagc	tgaaatttta	cacaaagcta	gatttagtta	catttttcga	240
218	attttggaa	tttgcata	gcctgaattt	ttgggaatag	ttactgaata	catgccaaat	300
219	ggatcattaa	atgaactctt	acataggaaa	actgaatatac	ctgtatgttc	ttggccattt	360
220	agatttcgca	tcctgcata	aatttgcctt	ggtgtaaatt	acctgcacaa	tatgactctt	420
221	ccttacttc	atcatgactt	gaagactcag	aatatcttat	tggacaatga	atttcatgtt	480
222	aagattgcag	attttggttt	atcaaagtgg	cgcataatgt	ccctctcaca	gtcacgaagt	540
223	agcaaatctg	caccagaagg	agggacaatt	atctatatgc	cacctgaaaa	ctatgaacct	600
224	ggacaaaaat	caagggccag	tatcaagcac	gatatatata	gctatgcagt	tatcataatgg	660
225	gaagtgttat	ccagaaaaca	gccttttggaa	gatgtcacca	atcccttgc	gataatgtat	720
226	agtgtgtcac	aaggacatcg	acctgttatt	aatgaagaaa	gtttgccata	tgtatatactt	780
227	caccgagcac	gtatgtatctc	tctaatagaa	agtggatggg	cacaaaatcc	agatggaaaaga	840
228	ccatctttct	taaaatgttt	aatagaactt	gaaccagttt	tgagaacatt	tgaagagata	900
229	actttcttg	aagctgttat	tcagctaaag	aaaacaaatgt	tacagagtgt	ttcaagtgcc	960
230	atcacctat	gtgacaagaa	gaaaatggaa	ttatctctga	acataccctgt	aatatcatgtt	1020
231	ccacaagagg	aatcatgtgg	atccctctcg	ctccatgaaa	atagtggttc	tcctgaaact	1080
232	tcaagggtccc	tgccagctcc	tcaagacaat	gatttttat	ctagaaaagc	tcaagactgt	1140
233	tattttatga	agctgcata	ctgtccctgg	aatcacatgt	gggatagcac	cattttctgg	1200
234	tctcaaagg	ctgcattctg	tgatcacaag	accattccat	gctttcagc	aataataat	1260
235	ccactctcaa	ctgcaggaaa	ctcagaacgt	ctgcagctg	gtatagccc	gcagtggatc	1320
236	cagagcaaaa	gggaagacat	tgtgaaccaa	atgacagaag	cctgccttaa	ccagtcgcta	1380
237	gatgcccttc	tgtccaggaa	cttgatcatg	aaagaggact	atgaacttgt	tagtaccaag	1440
238	cctacaagga	cctcaaaatgt	cagacaatta	ctagacacta	ctgacatcca	aggagaagaa	1500
239	tttgcctaaag	ttatagtaca	aaaattgaaa	gataacaaac	aaatgggtct	tcagccttac	1560
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242 <210> SEQ ID NO: 4
 243 <211> LENGTH: 300
 244 <212> TYPE: PRT
 245 <213> ORGANISM: Homo sapiens
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